AMENDMENT TO THE CLAIMS

This listing of claims will replace all prior versions of claims in the application.

Listing of Claims

1-78 (Cancelled)

79. (Currently Amended) A method for analyzing the toxicity of a test compound, said method comprising separately contacting, under conditions allowing hybridization to occur,

(a) first labeled nucleic acid probes, which are prepared or derived from mammalian cells contacted with said test compound, to ~~and~~ a library of nucleic acid molecules, wherein said library comprises, immobilized on a support, at least one nucleic acid molecule comprising the sequence set forth in SEQ ID NO: 16, and

(b) second labeled nucleic acid probes, which are prepared or derived from mammalian cells not contacted with said test compound, to ~~and~~ said nucleic acid library;

wherein said contacting steps (a) and (b) produce a first and a second hybridization profile, respectively, and detection of a difference between said first and second hybridization profiles indicates the toxicity of said test compound.

80. (Previously Presented) The method of claim 79, wherein the library comprises at least five nucleic acid molecules.

81. (Previously Presented) The method of claim 79, wherein said first and second nucleic probes of steps (a) and (b), respectively, correspond to messenger RNAs from cells contacted and not contacted with said test compound, respectively.

82. (Previously Presented) The method of claim 79, wherein said first and second nucleic probes of steps (a) and (b), respectively, are cDNA nucleic acid molecules or

cDNA nucleic acid molecule fragments prepared from RNA of cells contacted and not contacted with said test compound, respectively.

83. (Previously Presented) The method of claim 79, wherein said first and second nucleic probes of steps (a) and (b), respectively, are amplification products.

84. (Previously Presented) The method of claim 79, wherein said first and second nucleic probes of steps (a) and (b), respectively, are labeled by radioactive, fluorescent, enzymatic or colorimetric labels.

85. (Previously Presented) The method of claim 79, wherein the test compound is an individual compound or is present in a mixture of compounds.

86. (Previously Presented) The method of claim 79, wherein said library further comprises nucleic acid molecules specific for genes whose level of expression is modified in a cell which is undergoing or has undergone apoptosis.

87. (Previously Presented) The method of claim 79, wherein the cells contacted or not contacted with said test compound are of human origin.

88. (Previously Presented) The method of claim 79, wherein the cells contacted or not contacted with said test compound are cell lines.

89. (Previously Presented) The method of claim 79, wherein the cells contacted or not contacted with said test compound are primary cultures.

90. (Previously Presented) The method of claim 79, wherein said library of nucleic acid molecules is immobilized on a support.

91. (Previously Presented) The method of claim 90, wherein the support is selected from the group consisting of a filter, a membrane, a glass plate or a bio-chip.

92. (Previously Presented) The method of claim 79, wherein said first and second labeled nucleic acid probes are prepared or derived from a first and a second sample, respectively, comprising ribonucleic acid (RNA) molecules from mammalian cells contacted and not contacted, respectively, with said test compound.

93. (Currently Amended) A method for diagnosing the toxicity of a test compound, said method comprising contacting, under conditions allowing hybridization to occur:

(a) first labeled nucleic acid probes, which are prepared or derived from mammalian cells contacted with said test compound, to ~~and~~ a library of nucleic acid molecules, wherein said library comprises, immobilized on a support, at least one nucleic acid molecule comprising the sequence set forth in SEQ ID NO: 16, and

(b) second labeled nucleic acid probes, which are prepared or derived from mammalian cells not contacted with said test compound, to ~~and~~ said nucleic acid library;

wherein said contacting steps (a) and (b) produce a first and a second hybridization profile, respectively, and detection of a difference between said first and second hybridization profiles indicates the toxicity of said test compound.

94. (Currently Amended) A method for analyzing or determining the toxicity of a test compound, said method comprising separately contacting, under conditions allowing hybridization to occur,

(a) first labeled nucleic acid probes, which are prepared or derived from mammalian cells contacted with said test compound, to ~~and~~ a nucleic acid library, and

(b) second labeled nucleic acid probes, which are prepared or derived from mammalian cells not contacted with said test compound, to ~~and~~ said nucleic acid library;

wherein said nucleic acid library is immobilized on a support and consists essentially of marker nucleic acid molecules specific for all or a portion of one or more differentially spliced human genes present in a human cell which is undergoing or has undergone apoptosis and at least one or more control nucleic acid molecules which normalize the hybridization signals between said first and second labeled nucleic acid probes and said nucleic acid library, respectively, and

wherein said contacting steps (a) and (b) produce a first and a second hybridization profile, respectively, and detection of substantially equivalent hybridization signals between said first and second labeled nucleic acid probes and said control nucleic acid molecules, respectively, and of a difference in hybridization signals between said first and second labeled nucleic acid probes and said marker nucleic acid molecules in said first and second hybridization profiles indicates the toxicity of said test compound.

95. (Previously Presented) The method of claim 94, wherein said first and second nucleic acid probes of steps (a) and (b), respectively, correspond to messenger RNAs from cells contacted and not contacted with said test compound, respectively.

96. (Previously Presented) The method of claim 94, wherein said first and second nucleic acid probes of steps (a) and (b), respectively, are cDNA nucleic acid molecules or cDNA nucleic acid molecule fragments prepared from RNA obtained from cells contacted and not contacted with said test compound, respectively.

97. (Previously Presented) The method of claim 94, wherein said first and second nucleic acid probes of steps (a) and (b), respectively, are amplification products.

98. (Previously Presented) The method of claim 94, wherein said first and second nucleic acid probes of steps (a) and (b), respectively, are labeled by radioactive, fluorescent, enzymatic or colorimetric labels.

99. (Previously Presented) The method of claim 94, wherein the test compound is an individual compound or is present in a mixture of compounds.

100. (Previously Presented) The method of claim 94, wherein said marker nucleic acid molecules are specific for genes whose level of expression is modified in a cell which is undergoing or has undergone apoptosis.

101. (Previously Presented) The method of claim 94, wherein said nucleic acid library is prepared by (i) hybridizing a first nucleic acid population from a mammalian cell in a cell which is undergoing or has undergone apoptosis and a second nucleic acid population from a cell which is not undergoing or has not undergone apoptosis and (ii) separating, from the hybrids formed, nucleic acid molecules comprising an unpaired region.

102. (Previously Presented) The method of claim 101, wherein apoptosis is induced or enhanced in said mammalian cell.

103. (Previously Presented) The method of claim 102, wherein apoptosis is induced or enhanced by activation of the expression of an anti-oncogene.

104. (Previously Presented) The method of claim 103, wherein the anti-oncogene is selected from p53, Rb, p73, myc, TUPRO-2 and NHTS.

105. (Previously Presented) The method of claim 94, wherein said marker nucleic acid molecules are specific for at least a part of a gene selected from the following genes: Aldolase A; S4 subunit of proteasome 26S; Alpha-tubulin; Glucosidase II; lamin B receptor homologue; EF1-alpha; Fra-1; tyrosine kinase AX1 receptor; spliceosome Protein SAP62; TRAF-3; EF2; TEF-5; CDC25b; interleukine-1 receptor-associated kinase (IRAK); WAF-1; c-fos (exon 4); ckshs1; PL16; NFAR-2;

phosphatidylinositol4-kinase; ERF; Eph type receptor tyrosine kinase (hEphB1b); BAF60b protein of the SWI/SNF complex; EB1; MSS1; retinoic acid alpha receptor (RARa); translation initiation factor eiF4A; STE20 type kinase; protein HSP 90kda; Lipocortin II; translationally controlled tumor protein (TPTI); Hsc70; Cytokeratin 18; 2-oxoglutarate dehydrogenase; mitochondrial gene NADH6; mitochondrial gene NADH dehydrogenase 4; and alpha subunit of mitochondrial ATP synthase.

106-107 (Cancelled)

108. (Previously Presented) The method of claim 94, wherein the cells contacted or not contacted with said test compound are of human origin.

109. (Previously Presented) The method of claim 94, wherein the cells contacted or not contacted with said test compound are cell lines.

110. (Previously Presented) The method of claim 94, wherein the cells contacted or not contacted with said test compound are primary cultures.

111. (Previously Presented) The method of claim 94, wherein the support is selected from the group consisting of a filter, a membrane, a glass plate or a bio-chip.

112. (Previously Presented) The method of claim 94, wherein said first and second labeled nucleic acid probes are prepared or derived from a first and a second sample, respectively, comprising ribonucleic acid (RNA) molecules from mammalian cells contacted and not contacted, respectively, with said test compound.